SEQUENCE LISTING

<110> MacPhee, Colin Houston
     Tew, David Graham
     Southan, Christopher Donald
     Hickey, Deirdre Mary Bernadette
     Gloger, Israel Simon
     Lawrence, Geoffrey Mark Prouse
     Rice, Simon Quentyn John

<120> Lipoprotein Associated Phospholipase A2,
   Inhibitors Thereof and Use of the Same in Diagnosis and
   Therapy

<130> P30693C4X1C1

<140> 09/ 922,067
<141> 2001-08-03

<150> 09/193,130
<151> 2000-11-28

<150> 08/387,858
<151> 1994-06-24

<150> PCT/GB94/01374
<151> 1994-06-24

<150> GB 9313144.9
<151> 1993-06-25

<160> 11

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 37
<212> PRT
<213> Homo sapien

<400> 1
Met Leu Lys Leu Lys Gly Asp Ile Asp Ser Asn Ala Ala Ile Asp Leu
1   5   10   15

Ser Asn Lys Ala Ser Leu Ala Phe Leu Gln Lys His Leu Gly Leu His
                    20   25   30
Lys Asp Phe Asp Gln
            35

<210> 2
<211> 30
<212> PRT
<213> Homo sapien

<400> 2
Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile Pro Gln Pro
 1   5   10   15
Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala Asn
                20   25   30

<210> 3
<211> 27
<212> PRT
<213> Homo sapien

<400> 3
Gln Tyr Ile Asn Pro Ala Val Met Ile Thr Ile Arg Gly Ser Val His
 1   5   10   15
Gln Asn Phe Ala Asp Phe Thr Phe Ala Thr Gly
                20   25

<210> 4
<211> 19
<212> PRT
<213> Homo sapien

<400> 4
Trp Leu Met Gly Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr
 1   5   10   15
Pro Ala Asn

<210> 5
<211> 420

<212> DNA
<213> Unknown

<220>
<223> Where N can be represented by A, C, T, or G

<221> misc_feature
<222> 265, 390, 395, 403, 406
<223> n = A,T,C or G

<400> 5
aaaaaaccta ttttaatcct aattgtattt ctctattcct gaagagttct gtaacatgat 60
gtgttgattg gttgtgttaa tgttggtccc tggaataaga ttctcatcat ctccttcaat 120
caagcagtcc cactgatcaa aatctttatg aagtcctaaa tgcttttgta agaatgctaa 180
tgaagctttg ttgctaagat caatagctgc atttgaatct atgtctccct ttaatttgag 240
catgtgtcca attattttgc cagtngcaaa agtgaagtca gcaaaattct ggtggactga 300
acccctgatt gtaatcatct ttctttcttt atcaggtgag tagcattttt tcatttttat 360
gatattagca ggatattgga aatattcagn gttgntaaaa agnggnggct gagggattct 420

<210> 6
<211> 379
<212> DNA
<213> Unknown

<220>
<223> Where N can be represented by A, C, T, or G

<221> misc_feature
<222> 84
<223> n = A,T,C or G

<400> 6
tgctaatatc ataaaaatga aaaaatgcta ctcacctgat aaagaaagaa agatgattac 60
aatcaggggt tcagtccacc aganttttgc tgacttcact tttgcaactg gcaaaataat 120
tggacacatg ctcaaattaa agggagacat agattcaaat gtagctattg atcttagcaa 180
caaagcttca ttagcattct tacaaaagca tttaggactt cataaagatt ttgttcagtg 240
ggactgcttg attgaaggag atgatgagaa tcttattcca gggaccaaca ttaacacaac 300
caattcaaca catcatgttt acagaacttc ttccagggaa taggaggaaa tacaattggg 360
gtttaaaata ggttttttt 379

<210> 7
<211> 279
<212> DNA

<213> Unknown

<220>
<223> Where N can be represented by A, C, T, or G

<221> misc_feature
<222> 257
<223> n = A,T,C or G

<400> 7
gaagaatgca ttagatttaa agtttgatat ggaacaactg aaggactcta ttgataggga 60
aaaaatagca gtaattggac attctttttgg tggagcaacg gttattcaga ctcttagtga 120
agatcagaga ttcagatgtg gtattgccct ggatgcatgg atgtttccac tgggtgatga 180
agtatattcc agaattcctc agcccctctt ttttatcaac tctgaatatt tccaatatcc 240
tgctaatatc ataaaantgg aaaaatgcta ctcacctgg 279

<210> 8
<211> 572
<212> DNA
<213> Homo sapien

<400> 8
aaaatagcag taattggaca ttcttttaggt ggagcaacgg ttattcagac tcttagtgaa 60
gatcagagat tcagatgtgg tattgccctg gatgcatgga tgtttccact gggtgatgaa 120
gtatattcca gaattcctca gcccctcttt tttatcaact ctgaatattt ccaatatcct 180
gctaatatca taaaaatgaa aaaatgctac tcacctgata aagaagaaa gatgattaca 240
atcaggggtt cagtccacca gaattttgct gacttcactt ttgcaactgg caaaataatt 300
ggacacatgc tcaaattaaa gggagacata gattcaaatg tagctattga tcttagcaac 360
aaagcttcat cagcattctt acaaaagcat ttaggacttc ataaagattt tgatcagtgg 420
gactgcttga ttgaaggaga tgatgagaat cttattccag ggaccaacat taacacaacc 480
aatcaacaca tcatgttaca gaactcttca ggaatagaga aatacaatta ggattaaaat 540
aggtttttta aaaaaaaaaa aaaaaaaact cg 572

<210> 9
<211> 1361
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (38)...(1360)

<400> 9
tgagagacta agctgaaact gctgctcagc tcccaag atg gtg cca ccc aaa ttg 55

Met Val Pro Pro Lys Leu
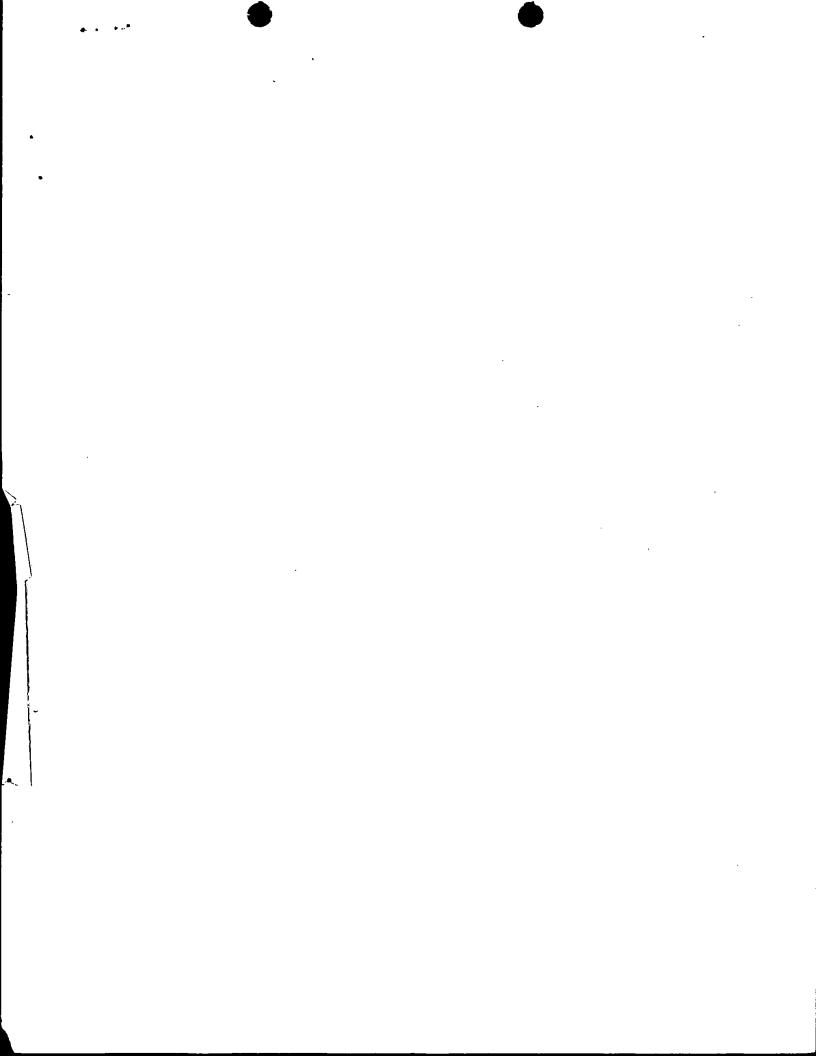   1   5

cat gtg ctt ttc tgc ctc tgc ggc tgc ctg gct gtg gtt tat cct ttt   103
His Val Leu Phe Cys Leu Cys Gly Cys Leu Ala Val Val Tyr Pro Phe
              10   15   20

gac tgg caa tac ata aat cct gtt gcc cat atg aaa tca tca gca tgg   151
Asp Trp Gln Tyr Ile Asn Pro Val Ala His Met Lys Ser Ser Ala Trp
          25   30   35

gtc aac aaa ata caa gta ctg atg gct gct gca agc ttt ggc caa act   199
Val Asn Lys Ile Gln Val Leu Met Ala Ala Ala Ser Phe Gly Gln Thr
      40   45   50

aaa atc ccc cgg gga aat ggg cct tat tcc gtt ggt tgt aca gac tta   247
Lys Ile Pro Arg Gly Asn Gly Pro Tyr Ser Val Gly Cys Thr Asp Leu
  55   60   65   70

atg ttt gat cac act aat aag ggc acc ttc ttg cgt tta tat tat cca   295
Met Phe Asp His Thr Asn Lys Gly Thr Phe Leu Arg Leu Tyr Tyr Pro
              75   80   85

tcc caa gat aat gat cgc ctt gac acc ctt tgg atc cca aat aaa gaa   343
Ser Gln Asp Asn Asp Arg Leu Asp Thr Leu Trp Ile Pro Asn Lys Glu
              90   95   100

tat ttt tgg ggt ctt agc aaa ttt ctt gga aca cac tgg ctt atg ggc   391
Tyr Phe Trp Gly Leu Ser Lys Phe Leu Gly Thr His Trp Leu Met Gly
          105   110   115

aac att ttg agg tta ctc ttt ggt tca atg aca act cct gca aac tgg   439
Asn Ile Leu Arg Leu Leu Phe Gly Ser Met Thr Thr Pro Ala Asn Trp
      120   125   130

aat tcc cct ctg agg cct ggt gaa aaa tat cca ctt gtt gtt ttt tct   487
Asn Ser Pro Leu Arg Pro Gly Glu Lys Tyr Pro Leu Val Val Phe Ser
135   140   145   150

cat ggt ctt ggg gca ttc agg aca ctt tat tct gct att ggc att gac   535
His Gly Leu Gly Ala Phe Arg Thr Leu Tyr Ser Ala Ile Gly Ile Asp
              155   160   165

ctg gca tct cat ggg ttt ata gtt gct gct gta gaa cac aga gat aga   583

```
Leu Ala Ser His Gly Phe Ile Val Ala Ala Val Glu His Arg Asp Arg
              170                     175                 180


tct gca tct gca act tac tat ttc aag gac caa tct gct gca gaa ata   631
Ser Ala Ser Ala Thr Tyr Tyr Phe Lys Asp Gln Ser Ala Ala Glu Ile
              185                     190                 195


ggg gac aag tct tgg ctc tac ctt aga acc ctg aaa caa gag gag gag   679
Gly Asp Lys Ser Trp Leu Tyr Leu Arg Thr Leu Lys Gln Glu Glu Glu
          200                     205                 210


aca cat ata cga aat gag cag gta cgg caa aga gca aaa gaa tgt tcc   727
Thr His Ile Arg Asn Glu Gln Val Arg Gln Arg Ala Lys Glu Cys Ser
215                     220                 225                 230


caa gct ctc agt ctg att ctt gac att gat cat gga aag cca gtg aag   775
Gln Ala Leu Ser Leu Ile Leu Asp Ile Asp His Gly Lys Pro Val Lys
                  235                 240                 245


aat gca tta gat tta aag ttt gat atg gaa caa ctg aag gac tct att   823
Asn Ala Leu Asp Leu Lys Phe Asp Met Glu Gln Leu Lys Asp Ser Ile
              250                     255                 260


gat agg gaa aaa ata gca gta att gga cat tct ttt ggt gga gca acg   871
Asp Arg Glu Lys Ile Ala Val Ile Gly His Ser Phe Gly Gly Ala Thr
          265                     270                 275


gtt att cag act ctt agt gaa gat cag aga ttc aga tgt ggt att gcc   919
Val Ile Gln Thr Leu Ser Glu Asp Gln Arg Phe Arg Cys Gly Ile Ala
          280                     285                 290


ctg gat gca tgg atg ttt cca ctg ggt gat gaa gta tat tcc aga att   967
Leu Asp Ala Trp Met Phe Pro Leu Gly Asp Glu Val Tyr Ser Arg Ile
295                     300                 305                 310


cct cag ccc ctc ttt ttt atc aac tct gaa tat ttc caa tat cct gct   1015
Pro Gln Pro Leu Phe Phe Ile Asn Ser Glu Tyr Phe Gln Tyr Pro Ala
                  315                 320                 325


aat atc ata aaa atg aaa aaa tgc tac tca cct gat aaa gaa aga aag   1063
Asn Ile Ile Lys Met Lys Lys Cys Tyr Ser Pro Asp Lys Glu Arg Lys
              330                     335                 340


atg att aca atc agg ggt tca gtc cac cag aat ttt gct gac ttc act   1111
```

```
Met Ile Thr Ile Arg Gly Ser Val His Gln Asn Phe Ala Asp Phe Thr
         345             350                 355


ttt gca act ggc aaa ata att gga cac atg ctc aaa tta aag gga gac    1159
Phe Ala Thr Gly Lys Ile Ile Gly His Met Leu Lys Leu Lys Gly Asp
         360             365                 370


ata gat tca aat gca gct att gat ctt agc aac aaa gct tca tta gca    1207
Ile Asp Ser Asn Ala Ala Ile Asp Leu Ser Asn Lys Ala Ser Leu Ala
375             380                 385                 390


ttc tta caa aag cat tta gga ctt cat aaa gat ttt gat cag tgg gac    1255
Phe Leu Gln Lys His Leu Gly Leu His Lys Asp Phe Asp Gln Trp Asp
             395                 400                 405


tgc ttg att gaa gga gat gat gag aat ctt att cca ggg acc aac att    1303
Cys Leu Ile Glu Gly Asp Asp Glu Asn Leu Ile Pro Gly Thr Asn Ile
             410                 415                 420


aac aca acc aat caa cac atc atg tta cag aac tct tca gga ata gag    1351
Asn Thr Thr Asn Gln His Ile Met Leu Gln Asn Ser Ser Gly Ile Glu
         425                 430                 435


aaa tac aat t                                                      1361
Lys Tyr Asn
         440



<210> 10
<211> 7
<212> PRT
<213> Homo sapien

<400> 10
Gln Tyr Ile Asn Pro Val Ala
 1               5



<210> 11
<211> 20
<212> PRT
<213> Homo sapien

<400> 11
```

Creation date: 10-01-2003
Indexing Officer: GMINIE - GELLA MINIE
Team: OIPEBackFileIndexing
Dossier: 09922067

Legal Date: 11-26-2001

No.	Doccode	Number of pages
1	CRFL	1

Total number of pages: 1

Remarks:

Order of re-scan issued on ....